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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Wed Jun 13 09:40:20 EDT 2007

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Application No: 10586045 Version No: 1.1

Input Set:

Output Set:

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Finished: 2007-06-13 09:40:03.821
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Total Errors: 0
No. of SeqIDs Defined: 45
Actual SeqID Count: 45

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Input Set:

Output Set:

Started: 2007-06-13 09:40:02.726
Finished: 2007-06-13 09:40:03.821
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 95 ms
Total Warnings: 31
Total Errors: 0
No. of SeqIDs Defined: 45
Actual SeqID Count: 45

Error code	Error Description
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SEQUENCE LISTING

<110> Korea Research Institute of Bioscience and Biotechnology
Sohn, Jung-Hoon
Choi, Eui-Sung
Bae, Jung-Hoon
Lee, Eung-Suck
Shin, Mi-Kyung

<120> Rapid screening method of translational fusion partners for
producing recombinant proteins and translational fusion partners
screened therefrom

<130> 2472.0010000

<140> US 10/586,045
<141> 2006-07-14

<150> PCT/KR2004/003517
<151> 2004-12-30

<150> KR 10-2004-0003610
<151> 2004-01-17

<150> KR 10-2004-0003957
<151> 2004-01-19

<160> 45

<170> PatentIn version 3.3

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<212> PRT
<213> Saccharomyces cerevisiae

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<221> PEPTIDE
<222> (1)..(105)
<223> TFP1

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Ala Asp Leu Ser Ser Ile Thr Ser Val Ser Ser Ala Ser Ala Ser Ala
35 40 45

Thr Ala Ser Asp Ser Leu Ser Ser Ser Asp Gly Thr Val Tyr Leu Pro

50

55

60

Ser Thr Thr Ile Ser Gly Asp Leu Thr Val Thr Gly Lys Val Ile Ala
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85 90 95

Gly Glu Lys Tyr Val Phe Ser Ser Asp
100 105

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aatcgaaaaa acaaattcca agctgctgtc gctttggccc tactctctcg cggcgctctc 180
ggtgactctt acaccaatag cacctccccc gcagacttga gttctatcac ttccgtctcg 240
tcagcttagtg caagtgccac cgcttccgac tcactttctt ccagtgacgg taccgtttat 300
ttgccatcca caacaattag cggtgatctc acagttactg gtaaaagtaat tgcaaccgag 360
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tcatctgatc 430

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<223> TFP2

<400> 3

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															30
Asn	Leu	Arg	Gly	Lys	Asn	Gly	Asp	Gly	Thr	Asn	Glu	Gln	Tyr	Ala	Thr
															45
Ala	Leu	Leu	Ser	Ile	Pro	Trp	Asn	Gly	Pro	Pro	Glu	Ser	Leu	Arg	Asp
50															60
Ile	Asn	Leu	Ile	Glu	Leu	Glu	Pro	Gln	Val	Ala	Leu	Tyr	Leu	Leu	Glu
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Asn	Tyr	Ile	Asn	His	Tyr	Tyr	Asn	Thr	Thr	Arg	Asp	Asn	Lys	Cys	Pro
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Arg	Ser	Leu	Asn	Asp											
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gtgagcgcac	tccaggtcaa	caattcatgt	gtcgctttc	cgcctatcaa	tctcagaggc	180
aaaaatggag	acggtaactaa	tgaacagtat	gcaactgcac	tactttctat	tccctggaat	240
ggacctcctg	agtcatgtgag	ggatattaat	cttattgaac	tgcgaccgca	agttgcactc	300
tatgtgctcg	aaaatttat	taaccattac	tacaacacca	caagagacaa	taagtgcct	360
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<223> TFP3

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Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
35 40 45

Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
50 55 60

Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
65 70 75 80

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85 90 95

Thr Pro Thr Ser Ser Glu Lys Ile
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acgtccacaa	acaaaaacaa	aaataagaaa	taggttgaca	gtgggtgaaa	aattctcgaa	180
ggtttcatct	ccaaacagtc	agtatataag	tattcggaa	agagagccaa	tctatcttgt	240
ggtgggtcta	tcttaacctt	ctcttttgg	cagtagtaat	tgttaatcaa	gacacataaa	300
actatttcac	tcgctaaact	tacatctaaa	atgcaattca	aaaacgtcgc	cctagctgcc	360
tccgttgctg	ctctatccgc	cactgcttct	gctgaagggtt	acactccagg	tgaaccatgg	420
tccaccttaa	cccccaaccgg	ctccatctct	tgtggtgctg	ccgaatacac	taccaccttt	480
ggtattgctg	ttcaagctat	tacctttca	aaagctaaga	gagacgttat	ctctcaaatt	540
ggtgacggtc	aagtccaagc	cacttctgct	gctactgctc	aagccaccga	tagtcaagcc	600
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 <213> Hansenula polymorpha

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 <222> (1)..(50)
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20															30

Gln	Met	Lys	Glu	Arg	Phe	Thr	Thr	Glu	Lys	Leu	Cys	Ala	Leu	Asp	Asp
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Lys Ile
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 <211> 179
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 <213> Hansenula polymorpha

<220>
<221> gene
<222> (1)..(179)
<223> TFP4

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ccacgttagg cggggggatg gctgcaccgg ttgagtc~~t~~ct ggccgggacc caacggtac 120
tggtgcaa~~a~~at gaaggagcgg ttcaccacag agaagctgtg tgcttgac gacaagatc 179

<210> 9
<211> 71
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<213> *Saccharomyces cerevisiae*

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<222> (1)..(71)
<223> TFP1-3

<400> 9

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20 25 30

Ala Asp Leu Ser Ser Ile Thr Ser Val Ser Ser Ala Ser Ala Ser Ala
35 40 45

Thr Ala Ser Asp Ser Leu Ser Ser Asp Gly Thr Val Tyr Leu Pro
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Ser Thr Thr Ile Ser Gly Asp
65 70

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acttccgtct cgtcagctag tgcaagtgcc accgcttcg actcactttc ttccagtgac 180

ggtaccgttt atttgccatc cacaacaatt agcggtgatc tcacagttac tggtaaagta 240

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aaatacgtct tctcatctga tcctctaga 329

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<213> Artificial Sequence

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<223> JH97 (Sfi-HSA-forward primer)

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<210> 12
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cggcccgagg cggccctaagg ctaaggcag 29

<210> 13
<211> 50
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<213> Artificial Sequence

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<223> JH99 (Sfi-INV-forward primer)

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gggcggccgc ctggcccta gataaaaaggta caatgacaaa cgaaacttagc 50

<210> 14
<211> 32
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<213> Artificial Sequence

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<223> JH100 (SalI-INV-reverse primer)

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<210> 15
<211> 37
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gcggccatta cggccgtgca cctacttcaa gttctac 37

<210> 16
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<212> DNA
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<223> JH107 (Sfi-IL2-reverse primer)

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gcggccatta cggccgtgca cctacttcaa gttctac 37

<210> 17
<211> 26
<212> DNA
<213> Artificial Sequence

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<223> JH120 (BamHI-IL2-1-forward primer)

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cgggatccgc acctacttca agttct 26

<210> 18
<211> 27
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<223> JH121 (BamHI-IL2-2-forward primer)

<400> 18
cgggatcctg cacctacttc aagttct 27

<210> 19
<211> 28
<212> DNA

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<223> JH122 (BamHI-IL2-3-forward primer)

<400> 19

cgggatcctt gcacctactt caagttct

28

<210> 20

<211> 22

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<223> JH123 (INV-1-reverse primer)

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ccattgaagg aaccaacaaa at

22

<210> 21

<211> 22

<212> DNA

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<223> JH124 (INV-forward primer)

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22

<210> 22

<211> 29

<212> DNA

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<223> JH95 (INV-2-reverse primer)

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<223> JH132 (SacI-GAL-forward primer)

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23

<210> 24
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<223> JH137 (IL-2-Term-reverse primer)

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<223> HY23 (TFP1-LDKR-forward primer)

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<223> HY20 (TFP2-LDKR-reverse primer)

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<210> 28
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46

<210> 29
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47

<210> 30
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27

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<223> JH142 (XbaI-TFP1-c-reverse primer)

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27

<210> 33
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<223> JH141 (XbaI-TFP1-b-reverse primer)

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cctctagaaac cgagagcgcc gcgagag

27

<210> 34

<211> 25

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<223> JH140 (SpeI-XbaI-LDKR-forward primer)

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ggactagtct agataaaagg gcacc

25

<210> 35

<211> 42

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<223> HY38 (TFP1-UTR-forward primer)

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<212> DNA

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<223> JH144 (GCSF-forward primer)

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<210> 38

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<210> 39

<211> 43

<212> DNA

<213> Artificial Sequence

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<223> HY18 (TFP3-LDKR-forward primer)

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<213> Saccharomyces cerevisiae

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20 25 30

Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
35 40 45

Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
50 55 60

Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
65 70 75 80

Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala
85 90 95

Thr Pro Thr Ser Ser Glu Lys Ile Ser Ser Ser Ala Ser Lys Thr Ser
100 105 110

Thr Asn Ala Thr Ser Ser Cys Ala Thr Pro Ser Leu Lys Asp Ser
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tgtggtgctg ccgaatacac taccaccttt ggtattgctg ttcaagctat tacctcttca 180

aaagctaaga gagacgttat ctctcaaatt ggtgacggtc aagtccaagc cacttctgct 240

gctactgctc aagccaccga tagtcaagcc caagctacta ctaccgctac cccaaaccagc 300

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Ala Thr Ala Ser Ala Glu Gly Tyr Thr Pro Gly Glu Pro Trp Ser Thr
20 25 30

Leu Thr Pro Thr Gly Ser Ile Ser Cys Gly Ala Ala Glu Tyr Thr Thr
35 40 45

Thr Phe Gly Ile Ala Val Gln Ala Ile Thr Ser Ser Lys Ala Lys Arg
50 55 60

Asp Val Ile Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Thr Ser Ala
65 70 75 80

Ala Thr Ala Gln Ala Thr Asp Ser Gln Ala Gln Ala Thr Thr Thr Ala
85 90 95

Thr Pro Thr Ser Ser Glu Lys Ile Ser Ser Ser Ala Ser Lys Thr Ser
100 105 110

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tgtggtgctg ccgaatacac ta